

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTRGQTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	100.0	114	4 AAB76942	Variable
2	596	100.0	114	8 ADN07029	Adn07029 Anti-IgE
3	596	100.0	114	9 ADW00651	Adw00651 Human ant
4	596	100.0	218	2 AAW95664	Aaw95664 Mus muscu
5	596	100.0	218	2 AAW95669	Aaw95669 Mus muscu
6	596	100.0	218	4 AAB47087	Aab47087 Anti-IgE
7	596	100.0	218	4 AAB76949	Aab76949 Full leng
8	596	100.0	218	4 AAB76951	Aab76951 Full leng
9	596	100.0	218	4 AAB76953	Aab76953 Variable
10	596	100.0	218	4 AAB76958	Aab76958 Variable
11	596	100.0	218	8 ADN07045	Adn07045 Anti-IgE
12	596	100.0	218	8 ADN07036	Adn07036 Anti-IgE
13	596	100.0	218	8 ADN07038	Adn07038 Anti-IgE
14	596	100.0	218	8 ADN07040	Adn07040 Anti-IgE
15	596	100.0	218	8 ADT55439	Adt55439 Anti IgE
16	596	100.0	218	9 ADW00660	Adw00660 Human ant
17	596	100.0	218	9 ADW00667	Adw00667 Human ant
18	596	100.0	218	9 ADW00662	Adw00662 Human ant
19	596	100.0	218	9 ADW00658	Adw00658 Human ant
20	596	100.0	218	9 ADW79897	Adw79897 Anti-IgE
21	596	100.0	218	9 ADW79902	Adw79902 Anti-IgE
22	596	100.0	218	9 AEB56305	Aeb56305 Anti-IgE
23	594	99.7	114	2 AAW95653	Aaw95653 Mus muscu
24	594	99.7	114	9 ADW79886	Adw79886 Anti-IgE

25	594	99.7	218	2 AAW95660	Aaw95660 Mus muscu
26	594	99.7	218	2 AAW95662	Aaw95662 Mus muscu
27	594	99.7	218	2 AAY50030	Aay50030 Human E27
28	594	99.7	218	3 AAB07472	Aab07472 Amino aci
29	594	99.7	218	4 AAB74211	Aab74211 E27 anti-
30	594	99.7	218	6 ABU62797	Abu62797 E27 anti-
31	594	99.7	218	7 ADP69597	Adp69597 Human ant
32	594	99.7	218	7 ADP29038	Adp29038 Anti-IgE
33	594	99.7	218	9 ADW79895	Adw79895 Anti-IgE
34	594	99.7	218	9 ADW79893	Adw79893 Anti-IgE
35	590	99.0	218	9 ADW00692	Adw00692 Human ant
36	587	98.5	248	2 AAW95668	Aaw95668 Mus muscu
37	587	98.5	248	2 AAW95667	Aaw95667 SPV fragm
38	587	98.5	248	4 AAB76956	Aab76956 SPV fragm
39	587	98.5	248	4 ADN07044	Adn07044 Anti-IgE
40	587	98.5	248	8 ADN07043	Adn07043 Anti-IgE
41	587	98.5	248	8 ADW00666	Adw00666 Human ant
42	587	98.5	248	9 ADW00665	Adw00665 Human ant
43	587	98.5	248	9 ADW79900	Adw79900 Anti-IgE
44	587	98.5	248	9 ADW79901	Adw79901 Anti-IgE
45	587	98.5	248	9 ADW79901	Adw79901 Anti-IgE

ALIGNMENTS

RESULT 1
AAB76942
ID AAB76942 standard; protein; 114 AA.
XX
AC AAB76942;
XX
DT 17-APR-2001 (first entry)
XX
DE Variable light chain sequence of e26 and e27 SEQ ID 8.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PE 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
(GETH) GENENTECH INC.
XX
Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
WPI; 2001-122353/13.
XX
New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phase display.
XX
XX
Disclosure; Fig 2; 87pp; English.
XX
This invention relates to a nucleotide sequence encoding an antibody with
XX improved anti-IgE antibody activity. The antibody has improved action due
XX to a process comprising, a) identifying aspartyl residues prone to
XX isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX substituting alternative residues to create candidate molecules; and c)
XX selecting those candidate molecules which display affinity against the
XX target molecule. Use of the antibody results in antiasthmatic;
XX anti-allergic; ophthalmological; dermatological and antiinflammatory
XX activity. The antibodies are useful for treating IgE-mediated disorders
XX such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and

CC food allergies. The mutant antibodies produced by the above mentioned
 CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 DB 1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 QY 61 GVPFRFSGSGTDTLTITSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPFRFSGSGTDTLTITSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 2
 ADN07029
 ID ADN07029 standard; protein; 114 AA.

XX AC ADN07029;

XX DT 01-JUL-2004 (first entry)

XX DE Anti-IgE antibody e26 and e27 variable light chain domain (VL).

XX KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 XX KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 XX KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 XX KW variable light chain domain; VL.

XX OS Unidentified.

XX FH Key Location/Qualifiers
 XX FT Region 24..40
 XX FT /label= CDR-L1
 XX FT Region 54..60
 XX FT /label= CDR-L2
 XX FT Region 93..100
 XX FT /label= CDR-L3

XX PN US6723833-B1.

XX PD 20-APR-2004.

XX PF 17-NOV-2000; 2000US-00716028.

XX PR 02-JUL-1997; 97US-0051554P.

XX PR 30-JUN-1996; 98US-00109207.

XX PA (GETH) GENENTECH INC.

XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX DR WPI; 2004-326922/30.

XX XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX PT conjunctivitis, eczema, urticaria or food allergies.

XX PS Disclosure; SEQ ID NO 8; 89pp; English.

XX CC The invention relates to therapeutic compositions comprising anti-IgE
 XX CC antibody or IgE binding fragment in combination with an adjunct
 XX CC immunosuppressive agent. The composition is useful for treating IgE-

CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain domain (VL).
 XX Sequence 114 AA;

Query Match 100.0%; Score 596; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.3e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 DB 1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 QY 61 GVPFRFSGSGTDTLTITSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPFRFSGSGTDTLTITSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 3
 ADW00651

ID ADW00651 standard; protein; 114 AA.

XX AC ADW00651;

XX DT 10-MAR-2005 (first entry)

XX DE Human anti-IgE antibody e26 and e27 light chain variable region protein.

XX KW Chemotherapy; IgE-mediated disorder; asthma; allergic rhinitis; eczema;
 XX KW urticaria; food allergy; hypersensitivity; anaphylactic hypersensitivity;
 XX KW antiasthmatic; antiallergic; dermatological; antibacterial;
 XX KW immune disorder; inflammation; ear disease; nose disease; throat disease;
 XX KW respiratory disease; antiinflammatory; dermatological disease;
 XX KW immunosuppressive; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Region 24..40
 XX FT /note= "CDR (Complementarity-determining region)-L1"

XX FT Region 54..60
 XX FT /note= "CDR (Complementarity-determining region)-L2"

XX FT Region 93..100
 XX FT /note= "CDR (Complementarity-determining region)-L3"

XX PN US2004259077-A1.

XX PD 23-DEC-2004.

XX PF 02-MAR-2004; 2004US-00791619.

XX PR 02-JUL-1997; 97US-0051554P.

XX PR 30-JUN-1998; 98US-00109207.

XX PR 17-NOV-2000; 2000US-00716028.

XX PA (GETH) GENENTECH INC.

XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX DR WPI; 2005-038757/04.

XX XX Treating an IgE-mediated disorder, e.g. asthma, allergic rhinitis,
 XX PT eczema, urticaria, food allergies, or hypersensitivity, by administering
 XX PT an anti-IgE antibody or its antigen-binding fragment.

XX PS Disclosure; SEQ ID NO 8; 92pp; English.

XX CC The present invention relates to a method for treating an IgE-mediated
 XX CC disorder. The method involves administering a therapeutical amount of an
 XX CC anti-IgE antibody or its IgE binding fragment. The invention is useful
 XX CC for treating an IgE-mediated disorder e.g. asthma, allergic rhinitis,

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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:31 ; Search time 19.3333 Seconds
(without alignments)
567.347 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTFGQTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	498	83.6	127	2 S40367	Ig kappa chain V-J
2	487	81.7	123	2 S40331	Ig kappa chain - h
3	486	81.5	108	2 B49047	Ig kappa chain V r
4	475	79.7	109	2 S31998	Ig kappa chain - h
5	471	79.0	108	2 S44122	Ig kappa chain V r
6	470	78.9	120	2 S46370	Ig kappa chain V-J
7	469	78.7	108	2 S47182	Ig kappa chain - h
8	468	78.5	109	2 S31981	Ig kappa chain - h
9	465.5	78.1	125	2 S40315	Ig kappa chain - h
10	464	77.9	108	1 KIHUHU	Ig kappa chain V-I
11	462	77.5	108	2 S19674	Ig kappa chain V r
12	462	77.5	122	2 S40370	Ig kappa chain - h
13	462	77.5	132	2 S40334	Ig kappa chain - h
14	461	77.3	129	2 S52793	Ig kappa chain V r
15	459	77.0	129	2 S52792	Ig kappa chain V r
16	458	76.8	107	2 S36264	Ig kappa chain V
17	457	76.7	117	2 S46371	Ig kappa chain V-J
18	457	76.7	122	2 S40314	Ig kappa chain - h
19	457	76.7	125	2 S40333	Ig kappa chain V-J
20	457	76.7	129	2 S40317	Ig kappa chain - h
21	456.5	76.6	124	2 S40336	Ig kappa chain V-J
22	456	76.5	108	1 KIHUDE	Ig kappa chain V-I
23	456	76.5	129	2 S40369	Ig kappa chain - h
24	456	76.5	131	2 S40352	Ig kappa chain V-J
25	455	76.3	109	2 S31978	Ig kappa chain - h
26	455	76.3	109	2 S31979	Ig kappa chain - h
27	454	76.2	125	2 S40350	Ig kappa chain pre
28	453	76.0	129	2 KIHUWK	Ig kappa chain V-J
29	452	75.8	126	2 S40335	Ig kappa chain V-J

30	451	75.7	109	2 S31980	Ig kappa chain - h
31	451	75.7	125	2 S40349	Ig kappa chain V-J
32	450	75.5	108	1 KIHUOU	Ig kappa chain V-I
33	450	75.5	130	2 S40368	Ig kappa chain - h
34	449.5	75.4	107	2 S36275	Ig lambda chain V
35	449	75.3	107	2 JLO139	Ig kappa chain V r
36	448	75.2	109	2 S32001	Ig kappa chain - h
37	448	75.2	109	2 S31983	Ig kappa chain - h
38	448	75.2	128	2 S46372	Ig light chain var
39	447	75.0	108	2 S31977	Ig kappa chain - h
40	447	75.0	117	2 S46376	Ig kappa chain V-J
41	447	75.0	125	2 S40316	Ig kappa chain - h
42	445	74.7	108	1 KIHUAV	Ig kappa chain V-I
43	445	74.7	108	1 KIHUBN	Ig kappa chain V-I
44	443	74.3	108	1 KIHULY	Ig kappa chain V-I
45	443	74.3	129	2 S52789	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 498; DB 2; Length 127;
Best Local Similarity 85.1%; Pred. No. 1.3e-36;
Matches 97; Conservative 8; Mismatches 5; Indels 4; Gaps 1;

QY	1	DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASVLES	60
Db	18	DIQMTQSPSSLSASVGDRTVITCRASQSI-----SNYLNWYQKPGKAPKLLIYAASLSQS	73
QY	61	GVPSRFSGSGGTDFLTITSSIQPEDFATYYCOQHEDPVTFGQTKVEIKRTV	114
Db	74	GVPSRFSGSGGTDFLTITSSIQPEDFATYYCOQSYNTPTWTFGQTKVEIKRTV	127

RESULT 2

S40331
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAA51109.1; P
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 487; DB 2; Length 123;

Best Local Similarity 86.5%; Pred. No. 1.1e-35;
Matches 96; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRDVTITCRASKPVDPGEBSYLNWYQKPGKAPKLLIYAASVLES 60
Db 17 DIQMTQSPSSLSASVGRDVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLSQS 72
Qy 61 GVPSRPSGSGSGTDFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIK 111
Db 73 GVPSRPSGSGSGTDFTLTISLQPEDPATYCCQSYSTRPTFGGTKVEIK 123

RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C/Species: Homo sapiens (man)
C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B49047
R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A/Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A/Reference number: A49047; MUID: 92387224; PMID: 1516616
A/Accession: B49047
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-108 <VIC>
A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A/Experimental source: thymic B lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 81.5%; Score 486; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.2e-35;
Matches 96; Conservative 5; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRDVTITCRASKPVDPGEBSYLNWYQKPGKAPKLLIYAASVLES 60
Db 1 DIQMTQSPSSLSASVGRDVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLSQS 56
Qy 61 GVPSRPSGSGSGTDFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKR 112
Db 57 GVPSRPSGSGSGTDFTLTISLQPEDPATYCCQSYSTRPTFGGTKVEIKR 108

RESULT 4
S31998
Ig kappa chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C/Accession: S31998
R/Portolano, S.; Chazenbalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A/Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A/Reference number: S31977
A/Accession: S31998
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-109 <PQR>
A/Cross-references: UNIPARC:UPI0000116497; EMBL:Z15081; NID:G38501; PIDN:CAA78790.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/16-90/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 475; DB 2; Length 109;
Best Local Similarity 80.5%; Pred. No. 1.1e-34;
Matches 91; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRDVTITCRASKPVDPGEBSYLNWYQKPGKAPKLLIYAASVLES 60
Db 1 ELVMTQSPSSLSASVGRDVTITCRASQSI-----SAYLNWYQKPGKAPKLLIYAASLSQS 56
Qy 61 GVPSRPSGSGSGTDFTLTISLQPEDPATYCCQSHEDPYTFGGTKVEIKRT 113

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTFQGTKEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	481	80.7	236	2	Q6GMX8_HUMAN
2	480	80.5	108	2	Q9UL77_HUMAN
3	470	78.9	236	2	Q6GMW1_HUMAN
4	468.5	78.6	107	2	Q96SA9_HUMAN
5	466	78.2	236	2	Q6GMX0_HUMAN
6	465	78.0	236	2	Q6PIH7_HUMAN
7	464	77.9	108	1	KV1H_HUMAN
8	456	76.5	108	1	KV1E_HUMAN
9	453	76.0	129	1	KV1W_HUMAN
10	450	75.5	108	1	KV1N_HUMAN
11	450	75.5	236	2	Q502W4_HUMAN
12	446	74.8	236	2	Q7Z3Y4_HUMAN
13	445	74.7	108	1	KV1B_HUMAN
14	445	74.7	108	1	KV1V_HUMAN
15	443.5	74.4	107	2	Q9UL81_HUMAN
16	443	74.3	108	1	KV1M_HUMAN
17	442	74.2	108	2	Q9UL70_HUMAN
18	442	74.2	234	2	Q7Z473_HUMAN
19	441	74.0	111	1	KV3M_MOUSE
20	440	73.8	108	1	KV1Q_HUMAN
21	440	73.8	108	1	KV1S_HUMAN
22	438	73.5	108	1	Q6GMX9_HUMAN
23	437	73.3	236	2	Q6GMX8_HUMAN
24	436	73.2	108	1	KV1F_HUMAN
25	436	73.2	108	1	KV1G_HUMAN
26	436	73.2	108	1	KV1V_HUMAN
27	436	73.2	111	1	KV3O_MOUSE
28	434	72.8	108	1	KV1P_HUMAN
29	434	72.8	111	1	KV3N_MOUSE
30	434	72.8	236	2	Q6PIT5_HUMAN
31	433	72.7	108	1	KV1R_HUMAN

32	433	72.7	111	1	KV3L_MOUSE	P01564 mus musculus
33	433	72.7	111	1	KV3Q_MOUSE	P01569 mus musculus
34	431	72.3	108	2	Q9UL79_HUMAN	Q9UL79 homo sapien
35	429	72.0	108	1	KVIL_HUMAN	P01604 homo sapien
36	429	72.0	234	2	Q5EFE6_HUMAN	Q5EFE6 homo sapien
37	429	72.0	236	2	Q6PIH4_HUMAN	Q6PIH4 homo sapien
38	428	71.8	189	2	Q569I7_HUMAN	Q569I7 homo sapien
39	427	71.6	116	2	Q96PF6_HUMAN	Q96PF6 homo sapien
40	427	71.6	244	2	Q65ZC8_HUMAN	Q65ZC8 homo sapien
41	425	71.3	108	1	KV1A_HUMAN	P01593 homo sapien
42	424.5	71.2	107	1	KV1D_HUMAN	P01596 homo sapien
43	423.5	71.1	109	1	KV1T_HUMAN	P01612 homo sapien
44	423	71.0	111	1	KV3H_MOUSE	P01660 mus musculus
45	423	71.0	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien

ALIGNMENTS

RESULT 1

Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8; DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RN [2]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH3764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B5559EFC9 CRC64;

Query Match 80.7%; Score 481; DB 2; Length 236;
Best Local Similarity 82.5%; Pred. No. 1.2e-39;
Matches 94; Conservative 9; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASLYLES 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQSI-----SSYLNWYQKPKAPKLLIYAASLYLES 78
Qy 61 GVPFRFSGSGGTDFTLTISSLPQEDPATYTCQSHEDPYTFGQGTKEIKRTV 114
Db 79 GVPFRFSGSGGTDFTLTISSLPQEDPATYTCQSHEDPYTFGQGTKEIKRTV 132

RESULT 2
Q5UL77_HUMAN PRELIMINARY; PRT; 108 AA.
AC Q5UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RA "Human monoclonal striational autoantibodies isolated from thymic B
RA lymphocytes of patients with myasthenia gravis use VH and VL gene
RA segments associated with the autoimmune repertoire.";
RA Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RA "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RA distributed over a large portion of the v kappa locus and do not show
RA somatic mutation.";
RA Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; 1BW.
DR SMR; Q5UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 80.5%; Score 480; DB 2; Length 108;
Best Local Similarity 83.9%; Pred. No. 6.3e-40;
Matches 94; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTSPSSLSASVGDRTVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASLYLES 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQSI-----SSYLNWYQKPKAPKLLIYAASLYLES 78
Qy 61 GVPFRFSGSGGTDFTLTISSLPQEDPATYTCQSHEDPYTFGQGTKEIKRTV 114
Db 79 GVPFRFSGSGGTDFTLTISSLPQEDPATYTCQSHEDPYTFGQGTKEIKRTV 132

RESULT 3
Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=24238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SMR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 78.9%; Score 470; DB 2; Length 236;
Best Local Similarity 82.3%; Pred. No. 1.5e-38;
Matches 93; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSLSASVGDRTV.....SHEDPYTFGGTKVEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5 COMB.pep: *
2: /cgn2_6/prodata/1/iaa/6 COMB.pep: *
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4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep: *
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6: /cgn2_6/prodata/1/iaa/backfilese1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	114	2	US-09-109-207C-8
2	596	100.0	114	2	US-09-296-005-8
3	596	100.0	114	2	US-09-920-171-8
4	596	100.0	114	2	US-09-716-028-8
5	596	100.0	114	2	US-10-113-996-8
6	596	100.0	218	1	US-08-887-352B-15
7	596	100.0	218	1	US-08-887-352B-17
8	596	100.0	218	1	US-08-887-352B-19
9	596	100.0	218	1	US-08-887-352B-24
10	596	100.0	218	2	US-09-109-207C-15
11	596	100.0	218	2	US-09-109-207C-17
12	596	100.0	218	2	US-09-109-207C-19
13	596	100.0	218	2	US-09-109-207C-24
14	596	100.0	218	2	US-09-296-005-15
15	596	100.0	218	2	US-09-296-005-17
16	596	100.0	218	2	US-09-296-005-19
17	596	100.0	218	2	US-09-296-005-24
18	596	100.0	218	2	US-09-920-171-15
19	596	100.0	218	2	US-09-920-171-17
20	596	100.0	218	2	US-09-920-171-19
21	596	100.0	218	2	US-09-920-171-24
22	596	100.0	218	2	US-09-716-028-15
23	596	100.0	218	2	US-09-716-028-17
24	596	100.0	218	2	US-09-716-028-19
25	596	100.0	218	2	US-09-716-028-24
26	596	100.0	218	2	US-10-113-996-15
27	596	100.0	218	2	US-10-113-996-17

28	596	100.0	218	2	US-10-113-996-19	Sequence 19, Appl
29	596	100.0	218	2	US-10-113-996-24	Sequence 24, Appl
30	594	99.7	114	1	US-08-887-352B-8	Sequence 8, Appl
31	594	99.7	218	2	US-09-282-505-1	Sequence 1, Appl
32	594	99.7	218	2	US-09-054-255-1	Sequence 1, Appl
33	594	99.7	218	2	US-09-282-846-1	Sequence 1, Appl
34	594	99.7	218	2	US-09-680-145-1	Sequence 1, Appl
35	594	99.7	218	2	US-09-483-588-1	Sequence 22, Appl
36	587	98.5	248	1	US-08-887-352B-22	Sequence 23, Appl
37	587	98.5	248	1	US-08-887-352B-23	Sequence 22, Appl
38	587	98.5	248	2	US-09-109-207C-22	Sequence 23, Appl
39	587	98.5	248	2	US-09-109-207C-23	Sequence 23, Appl
40	587	98.5	248	2	US-09-296-005-22	Sequence 23, Appl
41	587	98.5	248	2	US-09-296-005-23	Sequence 22, Appl
42	587	98.5	248	2	US-09-920-171-22	Sequence 23, Appl
43	587	98.5	248	2	US-09-920-171-23	Sequence 22, Appl
44	587	98.5	248	2	US-09-716-028-22	Sequence 22, Appl
45	587	98.5	248	2	US-09-716-028-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-09-109-207C-8
; Sequence 8, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Light chain sequence derived from MAB11
US-09-109-207C-8

Query Match	100.0%	Score 596;	DB 2;	Length 114;
Best Local Similarity	100.0%	Pred. No. 1.1e-49;	Mismatches 0;	Indels 0;
Matches 114;	Conservative 0;			Gaps 0;
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Db	1	DIQLTQSPSLSASVGDRTVITCRASKPVDGSDSYLNWYQQKPGKAPKLLIIYAASYLE 60		
QY	61	GVPSRFGSGSGTDFLTITSSLOPEDFATYVCOOSHEDPYTFGGTKVEIKRTV 114		
Db	61	GVPSRFGSGSGTDFLTITSSLOPEDFATYVCOOSHEDPYTFGGTKVEIKRTV 114		

RESULT 2

US-09-296-005-8
; Sequence 8, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 8

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; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 3
US-09-920-171-8
; Sequence 8, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P123C3US
; CURRENT APPLICATION NUMBER: US/09/920,171
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 4
US-09-716-028-8
; Sequence 8, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
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; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-716-028-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 5
US-10-113-996-8
; Sequence 8, Application US/10113996
; Patent No. 6761889
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US
; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-8

Query Match      100.0%; Score 596; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-49;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTV 114

RESULT 6
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....SHEDPYTFQGTKEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	114	3	US-09-920-171-8
2	596	100.0	114	4	US-10-113-996-8
3	596	100.0	114	5	US-10-791-619-8
4	596	100.0	218	3	US-09-920-171-15
5	596	100.0	218	3	US-09-920-171-17
6	596	100.0	218	3	US-09-920-171-19
7	596	100.0	218	3	US-09-920-171-24
8	596	100.0	218	4	US-10-113-996-15
9	596	100.0	218	4	US-10-113-996-17
10	596	100.0	218	4	US-10-113-996-19
11	596	100.0	218	4	US-10-113-996-24
12	596	100.0	218	4	US-10-813-483-2
13	596	100.0	218	5	US-10-791-619-15
14	596	100.0	218	5	US-10-791-619-17
15	596	100.0	218	5	US-10-791-619-19
16	596	100.0	218	5	US-10-791-619-24
17	596	100.0	218	5	US-10-714-000-1
18	596	100.0	218	5	US-10-698-073-12
19	596	100.0	218	5	US-10-698-073-17
20	596	100.0	218	6	US-11-013-966-2
21	594	99.7	114	5	US-10-698-073-1
22	594	99.7	218	3	US-09-792-938-1
23	594	99.7	218	4	US-10-292-869-1
24	594	99.7	218	4	US-10-835-642-1
25	594	99.7	218	5	US-10-757-863-1
26	594	99.7	218	5	US-10-698-073-8
27	594	99.7	218	5	US-10-698-073-10

28	594	99.7	218	5	US-10-982-470-1
29	594	99.7	218	6	US-11-158-839-1
30	587	98.5	248	3	US-09-920-171-22
31	587	98.5	248	3	US-09-920-171-23
32	587	98.5	248	4	US-10-113-996-22
33	587	98.5	248	4	US-10-113-996-23
34	587	98.5	248	5	US-10-791-619-22
35	587	98.5	248	5	US-10-791-619-23
36	587	98.5	248	5	US-10-698-073-15
37	587	98.5	248	5	US-10-698-073-16
38	575	96.5	114	3	US-09-920-171-9
39	575	96.5	114	4	US-10-113-996-9
40	575	96.5	114	5	US-10-791-619-9
41	573	96.1	114	5	US-10-698-073-2
42	570	95.6	114	3	US-09-920-171-10
43	570	95.6	114	4	US-10-113-996-10
44	570	95.6	114	5	US-10-791-619-10
45	570	95.6	114	5	US-10-698-073-3

ALIGNMENTS

RESULT 1

US-09-920-171-8
; Sequence 8, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-8

Query Match 100.0%; Score 596; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASVLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASVLES 60
QY 61 GVPFRFSGSGSGTDFLTITSSLPEDFATYCCQSHEDPYTFQGTKEIKRTV 114
Db 61 GVPFRFSGSGSGTDFLTITSSLPEDFATYCCQSHEDPYTFQGTKEIKRTV 114

RESULT 2

US-10-113-996-8
; Sequence 8, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C2US

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; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-113-996-8

Query Match      100.0%; Score 596; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

RESULT 3
US-10-791-619-8
; Sequence 8, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 8
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-10-791-619-8

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Best Local Similarity 100.0%; Pred. No. 2.7e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

RESULT 4
US-09-920-171-15
; Sequence 15, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-15

Query Match      100.0%; Score 596; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
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; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-15

Query Match      100.0%; Score 596; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

RESULT 5
US-09-920-171-17
; Sequence 17, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-17

Query Match      100.0%; Score 596; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

Qy 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
Db 61 GVPFRFSGSGGTDTLTLTSSQLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSLSASVGDRTV.....SHEDPYTFQGTKEIKRTV 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New.*
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2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pbp.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pbp.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pbp.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pbp.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pbp.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pbp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	100.0	218	US-10-923-327-12	Sequence 12, Appl
2	596	100.0	218	US-10-923-327-17	Sequence 17, Appl
3	594	99.7	114	US-10-923-327-1	Sequence 1, Appl
4	594	99.7	218	US-10-923-327-8	Sequence 8, Appl
5	594	99.7	218	US-10-923-327-10	Sequence 10, Appl
6	587	98.5	248	US-10-923-327-15	Sequence 15, Appl
7	587	98.5	248	US-10-923-327-16	Sequence 16, Appl
8	573	96.1	114	US-10-923-327-2	Sequence 2, Appl
9	570	95.6	114	US-10-923-327-3	Sequence 3, Appl
10	570	95.6	218	US-11-084-554-11	Sequence 11, Appl
11	562	94.3	218	US-10-923-327-6	Sequence 6, Appl
12	529	88.8	111	US-11-125-837-37	Sequence 37, Appl
13	494	82.9	111	US-11-077-978-1	Sequence 1, Appl
14	493	82.7	236	US-11-086-289-8	Sequence 8, Appl
15	492	82.6	108	US-10-925-366A-3	Sequence 3, Appl
16	492	82.6	108	US-10-925-366A-6	Sequence 6, Appl
17	492	82.6	240	US-10-925-366A-219	Sequence 219, Appl
18	490	82.2	214	US-11-128-900-71	Sequence 71, Appl
19	489	82.0	108	US-10-771-257-36	Sequence 36, Appl
20	489	82.0	108	US-11-127-677-36	Sequence 36, Appl
21	486	81.5	241	US-11-106-820-15	Sequence 15, Appl
22	485	81.4	107	US-11-064-174-156	Sequence 156, Appl
23	484	81.2	107	US-11-064-174-175	Sequence 175, Appl
24	484	81.2	107	US-11-064-174-176	Sequence 176, Appl
25	483	81.0	108	US-10-925-366A-156	Sequence 156, Appl

26	483	81.0	109	7	US-11-096-046-5	Sequence 5, Appl
27	482	80.9	108	6	US-10-925-366A-144	Sequence 144, App
28	482	80.9	108	6	US-10-925-366A-178	Sequence 178, App
29	482	80.9	108	6	US-10-925-366A-232	Sequence 232, App
30	481	80.7	109	6	US-10-834-397-28	Sequence 28, Appl
31	481	80.7	109	6	US-10-834-397-43	Sequence 43, Appl
32	480	80.5	108	6	US-10-925-366A-187	Sequence 187, Appl
33	480	80.5	108	6	US-10-925-366A-288	Sequence 288, App
34	480	80.5	114	6	US-10-925-366A-12	Sequence 12, Appl
35	479	80.4	107	7	US-11-064-174-179	Sequence 179, App
36	478	80.2	108	6	US-10-665-658-3	Sequence 3, Appl
37	478	80.2	108	7	US-11-120-338-3	Sequence 3, Appl
38	478	80.2	109	7	US-11-127-932-16	Sequence 16, Appl
39	478	80.2	109	7	US-11-127-932-17	Sequence 17, Appl
40	478	80.2	109	7	US-11-127-932-20	Sequence 20, Appl
41	478	80.2	109	7	US-11-127-903-16	Sequence 16, Appl
42	478	80.2	109	7	US-11-127-903-17	Sequence 17, Appl
43	478	80.2	109	7	US-11-127-903-20	Sequence 20, Appl
44	477	80.0	108	6	US-10-771-257-28	Sequence 28, Appl
45	477	80.0	108	6	US-10-834-397-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-923-327-12
; Sequence 12, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct

US-10-923-327-12
Query Match 100.0%; Score 596; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQLTQSPSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Db	1	DIQLTQSPSLSASVGDRTVITCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
Qy	61	GVPSRFGSGSGDFTLTITSSLOPEDFATYTCQSHEDPYTFQGTKEIKRTV 114
Db	61	GVPSRFGSGSGDFTLTITSSLOPEDFATYTCQSHEDPYTFQGTKEIKRTV 114

RESULT 2
US-10-923-327-17
; Sequence 17, Application US/10923327
; Publication No. US20050261208A1

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; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-17

Query Match      100.0%; Score 596; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
Db      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

Qy      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114
Db      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114

Qy      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114
Db      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114

RESULT 3
US-10-923-327-1
; Sequence 1, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-1

Query Match      99.7%; Score 594; DB 6; Length 114;
Best Local Similarity 99.1%; Pred. No. 1.5e-39;
Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
Db      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

Qy      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114
Db      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114

RESULT 5
US-10-923-327-10
; Sequence 10, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
;

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Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
Db      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

Qy      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114
Db      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114

RESULT 4
US-10-923-327-8
; Sequence 8, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-8

Query Match      99.7%; Score 594; DB 6; Length 218;
Best Local Similarity 99.1%; Pred. No. 2.5e-39;
Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
Db      1 DIQLTQSPSSLSASVGDRTTTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

Qy      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114
Db      61 GVPFRFSGSGSGTDTLTLTSSQLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTV 114

RESULT 5
US-10-923-327-10
; Sequence 10, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVQLVESGGGLVPGGSLRL.....YCARSGHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	2 AAW95656	Aaw95656 Mus muscu
2	623	100.0	114	4 AAB76945	Aab76945 Variable
3	623	100.0	114	8 ADN07032	Adn07032 Anti-IgE
4	623	100.0	114	9 ADW00654	Adw00654 Human ant
5	623	100.0	114	9 ADW79889	Adw79889 Anti-IgE
6	623	100.0	229	2 AAW95666	Aaw95666 Mus muscu
7	623	100.0	229	4 AAB76955	Aab76955 Variable
8	623	100.0	229	8 ADN07042	Adn07042 Anti-IgE
9	623	100.0	229	9 ADW00664	Adw00664 Human ant
10	623	100.0	229	9 ADW79899	Adw79899 Anti-IgE
11	623	100.0	233	2 AAW95671	Aaw95671 Mus muscu
12	623	100.0	233	4 AAB76960	Aab76960 Variable
13	623	100.0	233	8 ADN07047	Adn07047 Anti-IgE
14	623	100.0	233	9 ADW00669	Adw00669 Human ant
15	623	100.0	233	9 ADW79904	Adw79904 Anti-IgE
16	623	100.0	248	2 AAW95668	Aaw95668 Mus muscu
17	623	100.0	248	4 AAB76957	Aab76957 SVF fragm
18	623	100.0	248	8 ADN07044	Adn07044 Anti-IgE
19	623	100.0	248	9 ADW00666	Adw00666 Human ant
20	623	100.0	248	9 ADW79901	Adw79901 Anti-IgE
21	623	100.0	450	9 ADW79896	Adw79896 Anti-IgE
22	623	100.0	451	2 AAW95663	Aaw95663 Mus muscu
23	623	100.0	451	2 AAY50031	Aay50031 Human E27
24	623	100.0	451	3 AAB07473	Aab07473 Amino aci

25	623	100.0	451	4 AAB76952	Aab76952 Full leng
26	623	100.0	451	4 AAB74212	Aab74212 E27 anti-
27	623	100.0	451	6 ABE62798	Abe62798 E27 anti-
28	623	100.0	451	7 ADF69598	Adf69598 Human ant
29	623	100.0	451	7 ADF29039	Adf29039 Anti-IgE
30	623	100.0	451	8 ADN07039	Adn07039 Anti-IgE
31	623	100.0	451	8 ADW00661	Adw00661 Human ant
32	607	97.4	229	9 ADW00694	Adw00694 Human ant
33	603	96.8	114	2 AAW95657	Aaw95657 Mus muscu
34	603	96.8	114	4 AAB76946	Aab76946 Variable
35	603	96.8	114	8 ADN07033	Adn07033 Anti-IgE
36	603	96.8	114	9 ADW00655	Adw00655 Human ant
37	603	96.8	114	9 ADW79890	Adw79890 Anti-IgE
38	603	96.8	229	2 AAW95665	Aaw95665 Mus muscu
39	603	96.8	229	4 AAB76954	Aab76954 Variable
40	603	96.8	229	8 ADN07041	Adn07041 Anti-IgE
41	603	96.8	229	8 ADN07067	Adn07067 F(ab)-pha
42	603	96.8	229	9 ADW00663	Adw00663 Human ant
43	603	96.8	229	9 ADW00689	Adw00689 Expressio
44	603	96.8	229	9 ADW79898	Adw79898 Anti-IgE
45	603	96.8	233	2 AAW95670	Aaw95670 Mus muscu

ALIGNMENTS

RESULT 1

AAW95656
ID AAW95656 standard; protein; 114 AA.

AC AAW95656;

XX 08-JUN-1999 (first entry)

DE Mus musculus anti-IgE e27 variable heavy chain.

XX Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.

OS Mus musculus.

PN WO9901556-A2.

XX 14-JAN-1999.

PF 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

(GETH) GENENTECH INC.

PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

DR Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.

PS Disclosure; Page 90-91; 129pp; English.

CC The sequence is that of the variable heavy chain of e27. It was used as
CC part of a method to improve the affinity of anti-IgE antibodies such as
CC e26 and e27. The e26 and e27 antibodies can be used for reducing or
CC preventing IgE mediated production of histamine in a mammal. They can be
CC used for treating a disorder mediated by IgE such as hypersensitivity,
CC atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
CC eczema, anaphylactic shock and urticaria. The antibodies can also be used
CC for affinity purification, detection and diagnosis

XX

```

SQ Sequence 114 AA;
Query Match 100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 6e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60
Qy 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 2
AAB76945
ID AAB76945 standard; protein; 114 AA.
XX
AC AAB76945;
XX
DT 17-APR-2001 (first entry)
XX
DE Variable heavy chain sequence of e27 SEQ ID 11.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
WPI; 2001-122353/13.
XX
New nucleic acid encoding anti-immunoglobulin E antibody with improved
properties, produced by substituting aspartyl residues in unimproved
immunoglobulin E prone to isomerization by other residues by affinity
maturation with phage display.
XX
Disclosure; Fig 2; 87pp; English.
XX
This invention relates to a nucleotide sequence encoding an antibody with
improved anti-IgE antibody activity. The antibody has improved action due
to a process comprising, a) identifying aspartyl residues prone to
isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
substituting alternative residues to create candidate molecules; and c)
selecting those candidate molecules which display affinity against the
target molecule. Use of the antibody results in antiasthmatic;
antiallergic; ophthalmological; dermatological and antiinflammatory
activity. The antibodies are useful for treating IgE-mediated disorders
such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
food allergies. The mutant antibodies produced by the above mentioned
nucleic acids may also be used as affinity purification agents and in
diagnostic assays for detecting the expression of an antigen of interest
in specific cell, tissues or serum. Amino acid sequences AAB76936-
AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC Polynucleotide sequence AAB69233 represents an expression plasmid used in
CC the course of the invention, and oligonucleotides AAB69254 - AAB69271 are
CC used in the generation of affinity improved anti-IgE antibodies
XX
Sequence 114 AA;
Query Match 100.0%; Score 623; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 6e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 114 AA;
Query Match 100.0%; Score 623; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 6e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNIRQAPGKLEWVASIKYSGETKY 60
Qy 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 3
ADN07032
ID ADN07032 standard; protein; 114 AA.
XX
AC ADN07032;
XX
DT 01-JUL-2004 (first entry)
XX
DE Anti-IgE antibody e27 variable heavy chain domain (VH).
XX
KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
KW variable heavy chain domain; VH.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Region 26..36
FT /label= CDR-H1
FT Region 51..66
FT /label= CDR-H2
FT Region 99..110
FT /label= CDR-H3
XX
PN US6723833-B1.
XX
PD 20-APR-2004.
XX
PF 17-NOV-2000; 2000US-00716028.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PR 30-JUN-1998; 98US-00109207.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
WPI; 2004-326922/30.
XX
New composition of an improved anti-IgE antibody or IgE binding fragment,
useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
conjunctivitis, eczema, urticaria or food allergies.
XX
Disclosure; SEQ ID NO 11; 89pp; English.
XX
The invention relates to therapeutic compositions comprising anti-IgE
antibody or IgE binding fragment in combination with an adjunct
immunosuppressive agent. The composition is useful for treating IgE-
mediated disorders. The disorders include atopic allergy associated with
anaphylactic hypersensitivity and asthma, allergic rhinitis and
conjunctivitis, eczema, urticaria and food allergies. The present
sequence is an anti-IgE antibody variable heavy chain domain (VH).
XX
Sequence 114 AA;
Query Match 100.0%; Score 623; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 6e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Result No.	Score	Query #			DB	ID	Description
		Match	Length	Time			
1	419	67.3	140	2	S31588	Ig heavy chain v r	
2	418.5	67.2	140	2	S70442	Ig heavy chain pre	
3	418	67.1	123	2	S31114	Ig heavy chain - h	
4	416	66.8	138	2	S31666	Ig heavy chain v r	
5	413	66.3	121	2	S31113	Ig heavy chain - h	
6	411.5	66.1	147	2	S31780	Ig variable region	
7	409.5	65.7	122	2	E36005	Ig heavy chain v r	
8	409.5	65.7	128	2	S48797	Ig heavy chain v r	
9	409.5	65.7	141	2	S31669	Ig heavy chain v r	
10	408	65.5	125	2	S30531	Ig heavy chain v r	
11	407	65.3	117	2	S36259	Ig heavy chain v r	
12	407	65.3	119	2	S31107	Ig heavy chain - h	
13	404.5	64.9	122	2	S31117	Ig heavy chain - h	
14	404	64.8	121	2	S19666	Ig heavy chain v r	
15	404	64.8	121	2	G36005	Ig heavy chain v r	
16	404	64.8	135	2	S31598	Ig heavy chain v r	
17	404	64.8	140	2	S31686	Ig heavy chain v r	
18	403	64.7	127	2	S38489	Ig heavy chain - h	
19	401.5	64.4	137	2	S31701	Ig heavy chain v r	
20	401	64.4	123	2	S26794	Ig heavy chain v r	
21	400.5	64.3	124	2	S27882	Ig heavy chain v r	
22	399.5	64.1	114	2	S36280	Ig heavy chain v r	
23	399.5	64.1	136	2	S31587	Ig heavy chain v r	
24	399	64.0	119	2	S31108	Ig heavy chain - h	
25	399	64.0	160	2	S05271	Ig heavy chain pre	
26	398	63.9	119	2	D36005	Ig heavy chain v r	
27	398	63.9	143	2	S23624	Ig heavy chain v r	
28	397	63.7	112	2	S31603	Ig heavy chain v r	
29	396.5	63.6	116	2	S31110	Ig heavy chain - h	

Matches 83; Conservative 9; Mismatches 20; Indels 3; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-
 Db 20 QVQLVESGGGVVQPGGSLRLSCAASGFTF-SNYGMHVRQAPGKGLWVAFIRYDGSNKY 78

QY 60 YNPVSKGRITISRDDSKNTFLQMSLRADTA
 Db 79 YADSVKGRFTISRDNKNTLYLQMSLRADTA

RESULT 3
 S31114
 Ig heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S31114
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31114
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-123 <RAA>
 A:Cross-references: UNIPARC:UPI0000176C8A; EMBL:X62963
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 418; DB 2; Length 123;
 Best Local Similarity 71.8%; Pred. No. 2e-30;
 Matches 84; Conservative 11; Mismatches 18; Indels 4; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YAMSVWRQAPGKGLWVSAISGGSGTY 59

QY 60 YNPVSKGRITISRDDSKNTFLQMSLRADTA
 Db 60 YADSVKGRFTISRDNKNTLYLQMSLRADTA

RESULT 4
 S31666
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31666
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31666
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-138 <CUI>
 A:Cross-references: UNIPARC:UPI0000116474; EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 416; DB 2; Length 138;
 Best Local Similarity 70.4%; Pred. No. 3.3e-30;
 Matches 81; Conservative 15; Mismatches 15; Indels 4; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-
 Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YAMSVWRQAPGKGLWVSAISGGSGTY 78

QY 60 YNPVSKGRITISRDDSKNTFLQMSLRADTA
 Db 60 YADSVKGRFTISRDNKNTLYLQMSLRADTA

Db 79 YADSVKGRFTISRDNKNTLYLQMSLRADTA
 RESULT 5
 S31113
 Ig heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S31113
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31113
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-121 <RAA>
 A:Cross-references: UNIPARC:UPI0000176C89; EMBL:X62962
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 413; DB 2; Length 121;
 Best Local Similarity 70.4%; Pred. No. 5.4e-30;
 Matches 81; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-
 Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YAMSVWRQAPGKGLWVSAISGGSGTY 59

QY 60 YNPVSKGRITISRDDSKNTFLQMSLRADTA
 Db 60 YADSVKGRFTISRDNKNTLYLQMSLRADTA

RESULT 6
 I37780
 Ig variable region (VDJ) (clone T20-11) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
 C:Accession: I37780; S25474
 R:Denaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
 A:Reference number: A36876; MUID:94119917; PMID:8290556
 A:Accession: I37780
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-147 <RSS>
 A:Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:28-111/Domain: immunoglobulin homology <IMM>

Query Match 66.1%; Score 411.5; DB 2; Length 147;
 Best Local Similarity 70.3%; Pred. No. 9e-30;
 Matches 83; Conservative 12; Mismatches 18; Indels 5; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-
 Db 14 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YMWSVWRQAPGKGLWVANIKQDGSKY 72

QY 60 YNPVSKGRITISRDDSKNTFLQMSLRADTA
 Db 73 YADSVKGRFTISRDNKNTLYLQMSLRADTA

RESULT 7
 E36005
 Ig heavy chain V region (M72) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C:Accession: E36005

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVQLVESGGLVQPGSURL.....YCARSHYFGHWFAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413	66.3	470	Q6PJA4 HUMAN	Q6PJA4 homo sapien
2	408	65.5	113	Q9UL90 HUMAN	Q9UL90 homo sapien
3	404	64.8	479	Q5PQK9 RAT	Q5PQK9 rattus norv
4	399	64.0	466	Q6IN78 HUMAN	Q6IN78 homo sapien
5	398	63.9	478	Q6P181 HUMAN	Q6P181 homo sapien
6	397.5	63.8	118	Q9UL72 HUMAN	Q9UL72 homo sapien
7	396	63.6	120	Q9UL72 HUMAN	Q9UL72 homo sapien
8	394.5	63.3	613	Q8WUK1 HUMAN	Q8WUK1 homo sapien
9	394	63.2	240	Q652C9 HUMAN	Q652C9 homo sapien
10	393	63.2	472	Q6N089 HUMAN	Q6N089 homo sapien
11	393.5	63.2	122	Q9UL91 HUMAN	Q9UL91 homo sapien
12	392.5	63.0	118	Q9UL91 HUMAN	Q9UL91 homo sapien
13	391.5	62.8	467	Q4VBH1 RAT	Q4VBH1 rattus norv
14	391.5	62.8	473	Q6MZV7 HUMAN	Q6MZV7 homo sapien
15	391.5	62.8	606	Q6GMV2 HUMAN	Q6GMV2 homo sapien
16	391	62.8	597	Q96BB9 HUMAN	Q96BB9 homo sapien
17	389.5	62.5	475	Q6MZQ6 HUMAN	Q6MZQ6 homo sapien
18	389	62.4	116	Q9UL93 HUMAN	Q9UL93 homo sapien
19	389	62.4	121	Q9UL71 HUMAN	Q9UL71 homo sapien
20	389	62.4	464	Q6MZU6 HUMAN	Q6MZU6 homo sapien
21	385	61.8	123	Q9UL93 HUMAN	Q9UL93 homo sapien
22	384.5	61.7	116	Q9UL93 HUMAN	Q9UL93 homo sapien
23	383.5	61.6	573	Q8WU38 HUMAN	Q8WU38 homo sapien
24	382.5	61.4	147	Q9UL93 HUMAN	Q9UL93 homo sapien
25	382.5	61.4	470	Q4G060 RAT	Q4G060 rattus norv
26	382.5	61.4	478	Q5FVQ3 RAT	Q5FVQ3 rattus norv
27	382	61.3	117	Q9UL93 HUMAN	Q9UL93 homo sapien
28	381	61.2	493	Q6GMX2 HUMAN	Q6GMX2 homo sapien
29	380.5	61.1	494	Q96K68 HUMAN	Q96K68 homo sapien
30	377.5	60.6	112	Q9HCC1 HUMAN	Q9HCC1 homo sapien
31	377	60.5	468	Q569B4 RAT	Q569B4 rattus norv

32	377	60.5	493	2	Q8NCL6 HUMAN	Q8NCL6 homo sapien
33	374	60.0	115	1	Q9UL90 HUMAN	Q9UL90 homo sapien
34	374	60.0	123	1	Q9UL90 HUMAN	Q9UL90 homo sapien
35	374	60.0	499	1	Q8N5K4 HUMAN	Q8N5K4 homo sapien
36	372	59.7	119	1	Q9UL90 HUMAN	Q9UL90 homo sapien
37	371.5	59.6	465	2	Q5I0J0 RAT	Q5I0J0 rattus norv
38	371	59.6	487	2	Q8O2I7 MOUSE	Q8O2I7 mus musculu
39	370.5	59.5	469	2	Q569F4 HUMAN	Q569F4 homo sapien
40	370.5	59.5	483	2	Q5U413 MOUSE	Q5U413 mus musculu
41	370	59.4	121	1	Q9UL90 HUMAN	Q9UL90 homo sapien
42	369.5	59.3	119	2	Q5F2I8 MOUSE	Q5F2I8 mus musculu
43	369.5	59.3	122	1	Q9UL90 HUMAN	Q9UL90 homo sapien
44	368.5	59.1	461	2	Q5M7V3 RAT	Q5M7V3 rattus norv
45	368.5	59.1	479	2	Q6MZV6 HUMAN	Q6MZV6 homo sapien

ALIGNMENTS

RESULT 1
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH NCI Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SNR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.

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DR SMART, SM00406; IG, 1.
DR PROSITE, PS50835; IG LIKE; 4.
DR PROSITE, PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 66.3%; Score 413; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 3.2e-33;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVAIKYSGETKY 60
Db 20 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVAIKQDGSKY 78
QY 61 N-PSVKGRITTSRDDSKNTFYQMSLRADTAVYICAR-GSHYFGHHFPAVMGQ 114
Db 79 YVDSVKGRFTISRDNKNSLYLQMSLRADTAVYICARDGSSWTRDM-FDPWGQ 133

RESULT 2
Q9UL90 HUMAN
ID Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements."
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL, AF035024; RAD56260.1; -, mRNA.
DR FJ, S78486; S78486.
DR HSSP, P01772; 2FB4.
DR SMR, Q9UL90; 1-113.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART, SM00406; IG, 1.
DR PROSITE, PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.5%; Score 408; DB 2; Length 113;
Best Local Similarity 70.4%; Pred. No. 2.1e-33;
Matches 81; Conservative 10; Mismatches 14; Indels 10; Gaps 3;

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Db 1 EVQLVESGGGVVQPGSLRLSCAASGTFSS-YGMHWVQAPGKGLEWVAIFRYDGSNKY 59
QY 60 YNPVKGRITTSRDDSKNTFYQMSLRADTAVYICARGSHYFGHHFPAVMGQ 114
Db 60 YADSVKGRFTISRDNKNSLYLQMSLRADTAVYICARDLNY-----WGQ 106

us-10-791-619-11.rup

RESULT 3
Q5PQK9 RAT
ID Q5PQK9_RAT PRELIMINARY; PRT; 479 AA.
AC Q5PQK9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX NIH MGC Project;
RA EMBL; BC087137; AA87137.1; -, mRNA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR SMART, SM00409; IG; 3.
DR SMART, SM00406; IG, 1.
DR SMART, SM00406; IG, 1.
DR PROSITE, PS50835; IG LIKE; 3.
DR PROSITE, PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1652EF3457BE686E CRC64;

Query Match 64.8%; Score 404; DB 2; Length 479;
Best Local Similarity 68.7%; Pred. No. 2.7e-32;
Matches 79; Conservative 11; Mismatches 23; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVAIKYSGETK 59
Db 20 EVQLVESGGGLVQPGSLRLSCAASGTFSS-FNNYMTWIRQAPGKGLEWVAITNTGGKTY 78
QY 60 YNPVKGRITTSRDDSKNTFYQMSLRADTAVYICARGSHYFGHHFPAVMGQ 114
Db 79 YPDSVKGRFTISRDNKNSLYLQMSLRADTAVYICARAAHVMGPYYFAYWGQ 133

RESULT 4
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVOLVESGGGLVPGGSLRL.....YCARSHYFGHWHFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	1	US-08-887-352B-11
2	623	100.0	114	2	US-09-109-207C-11
3	623	100.0	114	2	US-09-296-005-11
4	623	100.0	114	2	US-09-920-171-11
5	623	100.0	114	2	US-09-716-028-11
6	623	100.0	114	2	US-10-113-996-11
7	623	100.0	229	1	US-08-887-352B-21
8	623	100.0	229	2	US-09-109-207C-21
9	623	100.0	229	2	US-09-296-005-21
10	623	100.0	229	2	US-09-920-171-21
11	623	100.0	229	2	US-09-716-028-21
12	623	100.0	229	2	US-10-113-996-21
13	623	100.0	233	1	US-08-887-352B-26
14	623	100.0	233	2	US-09-109-207C-26
15	623	100.0	233	2	US-09-296-005-26
16	623	100.0	233	2	US-09-920-171-26
17	623	100.0	233	2	US-09-716-028-26
18	623	100.0	233	2	US-10-113-996-26
19	623	100.0	248	1	US-08-887-352B-23
20	623	100.0	248	2	US-09-109-207C-23
21	623	100.0	248	2	US-09-296-005-23
22	623	100.0	248	2	US-09-920-171-23
23	623	100.0	248	2	US-09-716-028-23
24	623	100.0	248	2	US-10-113-996-23
25	623	100.0	451	1	US-08-887-352B-18
26	623	100.0	451	2	US-09-109-207C-18
27	623	100.0	451	2	US-09-282-505-2

28	623	100.0	451	2	US-09-054-255-2	Sequence 2, Appl
29	623	100.0	451	2	US-09-296-005-18	Sequence 18, Appl
30	623	100.0	451	2	US-09-282-846-2	Sequence 2, Appl
31	623	100.0	451	2	US-09-680-145-2	Sequence 2, Appl
32	623	100.0	451	2	US-09-920-171-18	Sequence 18, Appl
33	623	100.0	451	2	US-09-716-028-18	Sequence 18, Appl
34	623	100.0	451	2	US-09-483-588-2	Sequence 2, Appl
35	623	100.0	451	2	US-10-113-996-18	Sequence 18, Appl
36	603	96.8	114	1	US-08-887-352B-12	Sequence 12, Appl
37	603	96.8	114	2	US-09-109-207C-12	Sequence 12, Appl
38	603	96.8	114	2	US-09-296-005-12	Sequence 12, Appl
39	603	96.8	114	2	US-09-920-171-12	Sequence 12, Appl
40	603	96.8	114	2	US-09-716-028-12	Sequence 12, Appl
41	603	96.8	114	2	US-10-113-996-12	Sequence 12, Appl
42	603	96.8	229	1	US-08-887-352B-20	Sequence 20, Appl
43	603	96.8	229	2	US-09-109-207C-20	Sequence 20, Appl
44	603	96.8	229	2	US-09-296-005-20	Sequence 20, Appl
45	603	96.8	229	2	US-09-920-171-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-08-887-352B-11

; Sequence 11, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improved Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-887-352B-11

Query Match 100.0%; Score 623; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EVOLVESGGGLVPGGSLRLSCAVSGYSITSGYSWNMIROAPGKLEWVASIKYSGTKY	60
Db	1	EVOLVESGGGLVPGGSLRLSCAVSGYSITSGYSWNMIROAPGKLEWVASIKYSGTKY	60
Qy	61	NPSVKGRITISRDSDKNTFYQWNSLRADTVAVYCARSHYFGHWHFAVWGQ	114
Db	61	NPSVKGRITISRDSDKNTFYQWNSLRADTVAVYCARSHYFGHWHFAVWGQ	114

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RESULT 2
US-09-109-207C-11
; Sequence 11, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
QY 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114

RESULT 3
US-09-296-005-11
; Sequence 11, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
QY 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114

RESULT 4
US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
QY 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114

RESULT 5
US-09-716-028-11
; Sequence 11, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-11

Query Match      100.0%; Score 623; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.9e-55;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
DB 1 EVLVESGGGLVQPGGSLRLSCAAGYSSITSGYSNNWIRQAPGKLEWVASIKYSGTKY 60
QY 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114
DB 61 NPSVKGRITISRDDSKNTFYLQNSLRADTAIVYICARGSHYFGHWHFAVWGQ 114
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
Sequence: 1 EVOLVESGGLVPGGSLRL.....YCARSHYFGHWHFAVMGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	3	US-09-920-171-11
2	623	100.0	114	4	US-10-113-996-11
3	623	100.0	114	5	US-10-791-619-11
4	623	100.0	114	5	US-10-698-073-4
5	623	100.0	229	3	US-09-920-171-21
6	623	100.0	229	4	US-10-113-996-21
7	623	100.0	229	5	US-10-791-619-21
8	623	100.0	229	5	US-10-698-073-14
9	623	100.0	233	3	US-09-920-171-26
10	623	100.0	233	4	US-10-113-996-26
11	623	100.0	233	5	US-10-791-619-26
12	623	100.0	233	5	US-10-698-073-19
13	623	100.0	248	3	US-09-920-171-23
14	623	100.0	248	5	US-10-113-996-23
15	623	100.0	248	5	US-10-791-619-23
16	623	100.0	248	5	US-10-698-073-16
17	623	100.0	450	5	US-10-698-073-11
18	623	100.0	451	3	US-09-920-171-18
19	623	100.0	451	3	US-09-792-938-2
20	623	100.0	451	4	US-10-113-996-18
21	623	100.0	451	4	US-10-292-869-2
22	623	100.0	451	4	US-10-835-642-2
23	623	100.0	451	5	US-10-757-863-2
24	623	100.0	451	5	US-10-791-619-18
25	623	100.0	451	5	US-10-982-470-2
26	623	100.0	451	6	US-11-158-839-2
27	603	96.8	114	3	US-09-920-171-12

28	603	96.8	114	4	US-10-113-996-12	Sequence 12, Appl
29	603	96.8	114	5	US-10-791-619-12	Sequence 12, Appl
30	603	96.8	114	5	US-10-698-073-5	Sequence 5, Appl
31	603	96.8	229	3	US-09-920-171-20	Sequence 20, Appl
32	603	96.8	229	4	US-10-113-996-20	Sequence 20, Appl
33	603	96.8	229	5	US-10-791-619-20	Sequence 20, Appl
34	603	96.8	229	5	US-10-698-073-13	Sequence 13, Appl
35	603	96.8	233	3	US-09-920-171-25	Sequence 25, Appl
36	603	96.8	233	4	US-10-113-996-25	Sequence 25, Appl
37	603	96.8	233	5	US-10-791-619-25	Sequence 25, Appl
38	603	96.8	233	5	US-10-698-073-18	Sequence 18, Appl
39	603	96.8	248	3	US-09-920-171-22	Sequence 22, Appl
40	603	96.8	248	4	US-10-113-996-22	Sequence 22, Appl
41	603	96.8	248	5	US-10-791-619-22	Sequence 22, Appl
42	603	96.8	248	5	US-10-698-073-15	Sequence 15, Appl
43	603	96.8	451	3	US-09-920-171-14	Sequence 14, Appl
44	603	96.8	451	3	US-09-920-171-16	Sequence 16, Appl
45	603	96.8	451	3	US-09-925-179-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-09-920-171-11
; Sequence 11, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-11

Query Match	100.0%;	Score 623;	DB 3;	Length 114;
Best Local Similarity	100.0%;	Pred. No. 2.3e-51;		
Matches 114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVOLVESGGLVPGGSLRLSCAVSGYVTSITSGYSWNIROAPGKLEWVASIKYSGTKY	60	
Db	1	EVOLVESGGLVPGGSLRLSCAVSGYVTSITSGYSWNIROAPGKLEWVASIKYSGTKY	60	
Qy	61	NPSVKGRITISRDDSNTFFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVMGQG	114	
Db	61	NPSVKGRITISRDDSNTFFYLQNSLRAEDTAVVYCARGSHYFGHWHFAVMGQG	114	

RESULT 2
US-10-113-996-11
; Sequence 11, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US

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; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-11

Query Match      100.0%; Score 623; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 3
US-10-791-619-11
; Sequence 11, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 11
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-11

Query Match      100.0%; Score 623; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 4
US-10-698-073-4
; Sequence 4, Application US/10698073
; Publication No. US20050026881A1
; GENERAL INFORMATION:
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; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.201
; CURRENT APPLICATION NUMBER: US/10/698,073
; CURRENT FILING DATE: 2003-10-26
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-4

Query Match      100.0%; Score 623; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60
Db 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114

RESULT 5
US-09-920-171-21
; Sequence 21, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 21
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain F(ab) derived from MAE11
US-09-920-171-21

Query Match      100.0%; Score 623; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EVLVESGGGLVQPGGSLRLSCAAGSITSGYSNWIRQAPGKGLWVASIKYSGTKY 60

QY 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-11
Perfect score: 623
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
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 - 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
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 - 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	114	6	US-10-923-327-4
2	623	100.0	229	6	US-10-923-327-14
3	623	100.0	233	6	US-10-923-327-19
4	623	100.0	451	6	US-10-923-327-11
5	608	97.6	248	6	US-10-923-327-16
6	603	96.8	114	6	US-10-923-327-5
7	603	96.8	229	6	US-10-923-327-13
8	603	96.8	233	6	US-10-923-327-18
9	603	96.8	451	6	US-10-923-327-7
10	603	96.8	451	6	US-10-923-327-9
11	588	94.4	248	6	US-10-923-327-15
12	497	79.8	98	7	US-11-084-554-10
13	432	69.3	251	7	US-11-054-515-1114
14	428	68.7	248	7	US-11-054-515-1323
15	427	68.5	248	7	US-11-054-515-835
16	425	68.2	248	7	US-11-054-515-914
17	425	68.2	248	7	US-11-054-515-916
18	424.5	68.1	122	7	US-11-120-338-8
19	424.5	68.1	122	7	US-11-120-338-24
20	424.5	68.1	122	7	US-11-107-028-30
21	424.5	68.1	122	7	US-11-106-820-8
22	424.5	68.1	451	7	US-11-120-338-22
23	424.5	68.1	451	7	US-11-120-338-25
24	424.5	68.1	452	7	US-11-120-338-14
25	424.5	68.1	452	7	US-11-120-338-15

26	424.5	68.1	452	7	US-11-120-338-17	Sequence 17, Appl
27	424.5	68.1	452	7	US-11-107-028-32	Sequence 32, Appl
28	424.5	68.1	452	7	US-11-107-028-33	Sequence 33, Appl
29	424.5	68.1	452	7	US-11-107-028-47	Sequence 47, Appl
30	424.5	68.1	452	7	US-11-106-820-26	Sequence 26, Appl
31	424.5	68.1	452	7	US-11-106-820-28	Sequence 28, Appl
32	424.5	68.1	452	7	US-11-106-820-45	Sequence 45, Appl
33	424.5	68.1	471	7	US-11-106-820-25	Sequence 25, Appl
34	424.5	68.1	471	7	US-11-106-820-27	Sequence 27, Appl
35	424	68.1	129	6	US-10-850-635-12	Sequence 12, Appl
36	423	67.9	118	6	US-10-648-816-9	Sequence 9, Appl
37	423	67.9	118	6	US-10-648-816-14	Sequence 14, Appl
38	423	67.9	121	6	US-10-665-658-5	Sequence 5, Appl
39	423	67.9	121	6	US-11-107-028-50	Sequence 50, Appl
40	421.5	67.7	452	7	US-11-107-028-43	Sequence 43, Appl
41	421.5	67.7	452	7	US-11-107-028-45	Sequence 45, Appl
42	421.5	67.7	452	7	US-11-107-028-46	Sequence 46, Appl
43	421.5	67.7	452	7	US-11-106-820-30	Sequence 30, Appl
44	420.5	67.5	122	6	US-10-771-257-11	Sequence 11, Appl
45	420.5	67.5	122	7	US-11-127-677-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-923-327-4
; Sequence 4, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGF
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-923-327-4

Query Match 100.0%; Score 623; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.2e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITGSYNNWIRQAPCKGLEWVASIKYSGETKY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITGSYNNWIRQAPCKGLEWVASIKYSGETKY	60
QY	61	NPSVKGRITISRDDSKNTFYLNLSRAEDTAVVYCARGSHYFGHWHFAVWGQ	114
Db	61	NPSVKGRITISRDDSKNTFYLNLSRAEDTAVVYCARGSHYFGHWHFAVWGQ	114

RESULT 2
US-10-923-327-14
; Sequence 14, Application US/10923327
; Publication No. US20050261208A1

```

; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 14
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-14

Query Match          100.0%; Score 623; DB 6; Length 229;
Best Local Similarity 100.0%; Pred. No. 7.8e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

Qy      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 3
US-10-923-327-19
; Sequence 19, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-19

Query Match          100.0%; Score 623; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 8e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 4
US-10-923-327-11
; Sequence 11, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
;
US-10-923-327-11

Query Match          100.0%; Score 623; DB 6; Length 451;
Best Local Similarity 100.0%; Pred. No. 1.5e-46;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60
Db      1  EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVASIKYSGETKY 60

Qy      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114
Db      61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQG 114

RESULT 5
US-10-923-327-16
; Sequence 16, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:20:05 ; Search time 92.3333 Seconds
(without alignments)
542.482 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVQLVESGGLVPGGSLRL.....YCARSHYFHWFAVWGQ 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	100.0	114	2 AAW95657	Aaw95657 Mus muscu
2	625	100.0	114	4 AAB76946	Aab76946 Variable
3	625	100.0	114	8 ADN07033	Adn07033 Anti-IgE
4	625	100.0	114	9 ADW00655	Adw00655 Human ant
5	625	100.0	114	9 ADW79890	Adw79890 Anti-IgE
6	625	100.0	229	2 AAW95665	Aaw95665 Mus muscu
7	625	100.0	229	4 AAB76954	Aab76954 Variable
8	625	100.0	229	8 ADN07041	Adn07041 Anti-IgE
9	625	100.0	229	8 ADW07067	Adw07067 F(ab)-pha
10	625	100.0	229	9 ADW00663	Adw00663 Human ant
11	625	100.0	229	9 ADW00689	Adw00689 Expressio
12	625	100.0	229	9 ADW79898	Adw79898 Anti-IgE
13	625	100.0	233	2 AAW95670	Aaw95670 Mus muscu
14	625	100.0	233	4 AAB76959	Aab76959 Variable
15	625	100.0	233	8 ADN07046	Adn07046 Anti-IgE
16	625	100.0	233	9 ADW00668	Adw00668 Human ant
17	625	100.0	233	9 ADW79903	Adw79903 Anti-IgE
18	625	100.0	248	2 AAW95667	Aaw95667 Mus muscu
19	625	100.0	248	4 AAB76956	Aab76956 SFV fragm
20	625	100.0	248	8 ADN07043	Adn07043 Anti-IgE
21	625	100.0	248	8 ADW00665	Adw00665 Human ant
22	625	100.0	248	9 ADW79900	Adw79900 Anti-IgE
23	625	100.0	451	2 AAW95659	Aaw95659 Mus muscu
24	625	100.0	451	2 AAW95661	Aaw95661 Mus muscu

25	625	100.0	451	3 AAY85201	Aay85201 Light cha
26	625	100.0	451	4 AAB47088	Aab47088 Anti-IgE
27	625	100.0	451	4 AAB76948	Aab76948 Full leng
28	625	100.0	451	4 AAB76950	Aab76950 Full leng
29	625	100.0	451	8 ADN07037	Adn07037 Anti-IgE
30	625	100.0	451	8 ADN07035	Adn07035 Anti-IgE
31	625	100.0	451	8 ADT55442	Adt55442 Anti-IgE
32	625	100.0	451	8 ADT55441	Adt55441 Anti-IgE
33	625	100.0	451	8 ADW00659	Adw00659 Human ant
34	625	100.0	451	9 ADW00657	Adw00657 Human ant
35	625	100.0	451	9 ADW79892	Adw79892 Anti-IgE
36	625	100.0	451	9 ADW79894	Adw79894 Anti-IgE
37	625	100.0	451	9 AEB56308	Aeb56308 Anti-IgE
38	625	100.0	451	9 AEB56307	Aeb56307 Anti-IgE
39	625	100.0	474	8 ADQ90734	Adq90734 Anti-IgE
40	609	97.4	229	9 ADW00693	Adw00693 Human ant
41	605	96.8	121	2 AAW95648	Aaw95648 Mus muscu
42	605	96.8	121	4 AAB76937	Aab76937 Variable
43	605	96.8	121	8 ADN07024	Adn07024 Murine an
44	605	96.8	121	9 ADW00646	Adw00646 Human F(a
45	605	96.8	453	2 AAR33311	Aar33311 Humanised

ALIGNMENTS

RESULT 1
AAW95657
ID AAW95657 standard; protein; 114 AA.

XX AAW95657;

XX 08-JUN-1999 (first entry)

XX Mus musculus anti-IgE e25, e26 & e426 variable heavy chain.

XX Variable heavy chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; IgE; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.

XX Mus musculus.

XX WO9901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

XX (GETH) GENENTECH INC.

XX Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
target.

XX Disclosure; Page 91; 129pp; English.

XX The sequence is that of the variable heavy chain of e25, e26 and e426. It
was used as part of a method to improve the affinity of anti-IgE
antibodies such as e26 and e27. The e26 and e27 antibodies can be used
for reducing or preventing IgE mediated production of histamine in a
mammal. They can be used for treating a disorder mediated by IgE such as
CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
antibodies can also be used for affinity purification, detection and
diagnosis

XX SQ Sequence 114 AA;
 Query Match 100.0%; Score 625; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.1e-50;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
 QY 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 DB 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 RESULT 2
 AAB76946
 ID AAB76946 standard; protein; 114 AA.
 XX AC AAB76946;
 XX DT 17-APR-2001 (first entry)
 XX DE Variable heavy chain sequence of e25, e26 and e426 SEQ ID 12.
 XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 XX KW conjunctivitis; eczema; urticaria; food allergy.
 XX OS Synthetic.
 XX FH US6172213-B1.
 XX FT 09-JAN-2001.
 XX PD 30-JUN-1998; 98US-00109207.
 XX PF 02-JUL-1997; 97US-0051554P.
 XX PR (GETH) GENENTECH INC.
 XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX PI WPI; 2001-122353/13.
 XX DR New nucleic acid encoding anti-immunoglobulin E antibody with improved
 XX PT properties, produced by substituting aspartyl residues in unimproved
 XX PT immunoglobulin E prone to isomerization by other residues by affinity
 XX PT maturation with phage display.
 XX PS Disclosure; Fig 2; 87pp; English.
 XX CC This invention relates to a nucleotide sequence encoding an antibody with
 XX CC improved anti-IgE antibody activity. The antibody has improved action due
 XX CC to a process comprising, a) identifying aspartyl residues prone to
 XX CC isomerization in unimproved anti-IgE (immunoglobulin E) antibody; b)
 XX CC substituting alternative residues to create candidate molecules, and c)
 XX CC selecting those candidate molecules which display affinity against the
 XX CC target molecule. Use of the antibody results in antiasthmatic;
 XX CC antiallergic; ophthalmological; dermatological and antiinflammatory
 XX CC activity. The antibodies are useful for treating IgE-mediated disorders
 XX CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
 XX CC food allergies. The mutant antibodies produced by the above mentioned
 XX CC nucleic acids may also be used as affinity purification agents and in
 XX CC diagnostic assays for detecting the expression of an antigen of interest
 XX CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 XX CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 XX CC Polynucleotide sequence AAB69253 represents an expression plasmid used in
 XX CC the course of the invention, and oligonucleotides AAB69254 - AAB69271 are
 XX CC used in the generation of affinity improved anti-IgE antibodies
 XX SQ Sequence 114 AA;

Query Match 100.0%; Score 625; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.1e-50;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTNY 60
 QY 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 DB 61 NPSVKGRITISRDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
 RESULT 3
 ADN07033
 ID ADN07033 standard; protein; 114 AA.
 XX AC ADN07033;
 XX DT 01-JUL-2004 (first entry)
 XX DE Anti-IgE antibody e25, e26 and e426 variable heavy chain domain (VH).
 XX KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 XX KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 XX KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 XX KW variable heavy chain domain; VH.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 XX FT Region 26..36
 XX FT /label= CDR-H1
 XX FT Region 51..66
 XX FT /label= CDR-H2
 XX FT Region 99..110
 XX FT /label= CDR-H3
 XX PN US6723833-B1.
 XX PD 20-APR-2004.
 XX PF 17-NOV-2000; 2000US-00716028.
 XX PR 02-JUL-1997; 97US-0051554P.
 XX PR 30-JUN-1998; 98US-00109207.
 XX PA (GETH) GENENTECH INC.
 XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX PI WPI; 2004-326922/30.
 XX DR New composition of an improved anti-IgE antibody or IgE binding fragment,
 XX PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 XX PT conjunctivitis, eczema, urticaria or food allergies.
 XX PS Disclosure; SEQ ID NO 12; 89pp; English.
 XX CC The invention relates to therapeutic compositions comprising anti-IgE
 XX CC antibody or IgE binding fragment in combination with an adjunct
 XX CC immunosuppressive agent. The composition is useful for treating IgE-
 XX CC mediated disorders. The disorders include atopic allergy associated with
 XX CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 XX CC conjunctivitis, eczema, urticaria and food allergies. The present
 XX CC sequence is an anti-IgE antibody variable heavy chain domain (VH).
 XX SQ Sequence 114 AA;
 Query Match 100.0%; Score 625; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.1e-50;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	420.5	67.3	140	2	S70442	Ig heavy chain pre
2	420	67.2	140	2	S31588	Ig heavy chain v r
3	419	67.0	123	2	S31114	Ig heavy chain - h
4	417	66.7	138	2	S31666	Ig heavy chain v r
5	415.5	66.5	122	2	E36005	Ig heavy chain v r
6	415.5	66.5	128	2	S48797	Ig heavy chain v r
7	414	66.2	121	2	S31113	Ig heavy chain - h
8	410.5	65.7	122	2	S31117	Ig heavy chain - h
9	410.5	65.7	141	2	S33669	Ig heavy chain v r
10	410.5	65.7	147	2	S37780	Ig variable region
11	410	65.6	121	2	S19666	Ig heavy chain v r
12	410	65.6	121	2	G36005	Ig heavy chain v r
13	409	65.4	117	2	S36259	Ig heavy chain v r
14	409	65.4	125	2	S30531	Ig heavy chain v r
15	408	65.3	119	2	S31107	Ig heavy chain - h
16	407.5	65.2	137	2	S31701	Ig heavy chain v r
17	406	65.0	135	2	S31598	Ig heavy chain v r
18	405	64.8	140	2	S31686	Ig heavy chain v r
19	404	64.6	127	2	S39489	Ig heavy chain - h
20	403	64.5	132	2	S33603	Ig heavy chain v r
21	402	64.3	123	2	S26794	Ig heavy chain v r
22	402	64.3	130	2	S33601	Ig heavy chain v r
23	401.5	64.2	118	2	S31116	Ig heavy chain - h
24	401.5	64.2	139	2	S31674	Ig heavy chain v r
25	400.5	64.1	114	2	S46390	Ig heavy chain v r
26	400	64.0	119	2	S33108	Ig heavy chain - h
27	400	64.0	119	2	F36005	Ig heavy chain v r
28	400	64.0	134	2	S33679	Ig heavy chain v r
29	400	64.0	160	2	S05271	Ig heavy chain pre

Query Match 87.2%, Score 420, SS 2, Length 110
Best Local Similarity 71.3%; Pred. No. 5.3e-30;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:24:05 ; Search time 101.667 Seconds
(without alignments)
791.117 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVQLVESGGLVPGGSLRL.....YCARGSHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	412	65.9	470	2 Q6PJA4 HUMAN	Q6PJA4 homo sapien
2	411	65.8	479	2 Q5PQK9 RAT	Q5PQK9 rattus norv
3	410	65.6	113	2 Q9UL90 HUMAN	Q9UL90 homo sapien
4	403.5	64.6	118	2 Q9UL72 HUMAN	Q9UL72 homo sapien
5	400.5	64.1	467	2 Q4VBH1 RAT	Q4VBH1 rattus norv
6	400.5	64.1	613	2 Q8WUK1 HUMAN	Q8WUK1 homo sapien
7	400	64.0	121	2 Q9UL71 HUMAN	Q9UL71 homo sapien
8	400	64.0	240	2 Q652C9 HUMAN	Q652C9 homo sapien
9	400	64.0	466	2 Q6IN78 HUMAN	Q6IN78 homo sapien
10	398.5	63.8	606	2 Q6GMV2 HUMAN	Q6GMV2 homo sapien
11	397	63.5	478	2 Q6PI81 HUMAN	Q6PI81 homo sapien
12	395	63.2	116	2 Q9UL93 HUMAN	Q9UL93 homo sapien
13	395	63.2	472	2 Q6N089 HUMAN	Q6N089 homo sapien
14	394.5	63.1	473	2 Q6MZV7 HUMAN	Q6MZV7 homo sapien
15	393.5	63.0	118	2 Q9UL91 HUMAN	Q9UL91 homo sapien
16	392.5	62.8	122	1 HV3G HUMAN	HV3G homo sapien
17	392.5	62.8	147	2 Q9Y509 HUMAN	Q9Y509 homo sapien
18	392	62.7	493	2 Q6GMX2 HUMAN	Q6GMX2 homo sapien
19	392	62.7	597	2 Q96BB9 HUMAN	Q96BB9 homo sapien
20	391	62.6	120	1 HV3E HUMAN	HV3E homo sapien
21	391	62.6	464	2 Q6MZU6 HUMAN	Q6MZU6 homo sapien
22	390	62.4	123	1 HV24 MOUSE	HV24 mus musculus
23	387.5	62.0	116	1 HV05 CARAU	P19181 carassius a
24	387.5	62.0	475	2 Q6MZQ6 HUMAN	Q6MZQ6 homo sapien
25	387.5	62.0	573	2 Q8WU38 HUMAN	Q8WU38 homo sapien
26	384	61.4	493	2 Q8NCL6 HUMAN	Q8NCL6 homo sapien
27	384	61.4	499	2 Q8NSK4 HUMAN	Q8NSK4 homo sapien
28	383.5	61.4	112	2 Q9HCCL HUMAN	Q9HCCL homo sapien
29	383	61.3	117	1 HV3C HUMAN	P01764 homo sapien
30	381.5	61.0	469	2 Q569F4 HUMAN	Q569F4 homo sapien
31	380.5	60.9	119	2 Q5F218 MOUSE	Q5F218 mus musculus

32	380.5	60.9	461	2 Q5M7V3 RAT	Q5M7V3 rattus norv
33	380.5	60.9	465	2 Q5I0J0 RAT	Q5I0J0 rattus norv
34	380	60.8	119	2 Q53VQ5 MOUSE	Q53VQ5 mus musculus
35	379	60.6	479	2 Q99M22 MOUSE	Q99M22 mus musculus
36	378.5	60.6	470	2 Q4G060 RAT	Q4G060 rattus norv
37	378.5	60.6	494	2 Q96K68 HUMAN	Q96K68 homo sapien
38	377.5	60.4	478	2 Q5FVQ3 RAT	Q5FVQ3 rattus norv
39	377.5	60.4	483	2 Q5U413 MOUSE	Q5U413 mus musculus
40	377	60.3	468	2 Q589B4 RAT	Q589B4 rattus norv
41	376	60.2	479	2 Q5BK12 RAT	Q5BK12 rattus norv
42	375	60.0	115	1 HV3F HUMAN	P01767 homo sapien
43	375	60.0	121	1 HV3J HUMAN	P01771 homo sapien
44	375	60.0	123	1 HV22 MOUSE	P01791 mus musculus
45	374.5	59.9	119	1 HV37 MOUSE	P01807 mus musculus

ALIGNMENTS

RESULT 1
Q6PJA4_HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Browne M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
NIH MGC Project;
R Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Query Match 65.9%; Score 412; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 3.3e-32;
Matches 84; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITVDGSTNY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVSGTFS-YNMSWVRQAPGKLEWVANI KODGSEKY 78
QY 61 N-PSVKGRITISRDSDSKNTFYLQMSLRADTAIVYCAR-GSHYFGHWHFAVMGQ 114
DB 79 YDVSVKGRFTISRDNAKNSLYLQMSLRADTAIVYCARDGSSWYRDW-FDPWGQ 133

RESULT 2
QSPQK9 RAT
ID QSPQK9_RAT PRELIMINARY; PRT; 479 AA.
AC QSPQK9;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Igha protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087137; AAH87137.1; -; mRNA.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 479 AA; 52354 MW; 1692EF3457BE686E CRC64;

Query Match 65.8%; Score 411; DB 2; Length 479;
Best Local Similarity 69.6%; Pred. No. 4.3e-32;
Matches 80; Conservative 10; Mismatches 23; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITVDGSTNY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCVSGTFS-NNYMTWIRQAPGKLEWVASITVDGKTY 78
QY 61 NP-SVKGRITISRDSDSKNTFYLQMSLRADTAIVYCAR-GSHYFGHWHFAVMGQ 114
DB 79 YPDSVKGRFTISRDNAKSTLYLQMSLRSDTATYCTRAAHVMPGYVFAVMGQ 133

RESULT 3
Q9UL90 HUMAN
ID Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cllin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Rasphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
complementarity-determining regions (CDR3) in human fetal B lymphocyte
immunoglobulin heavy chain rearrangements."
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 113
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 65.6%; Score 410; DB 2; Length 113;
Best Local Similarity 71.3%; Pred. No. 1.1e-32;
Matches 82; Conservative 9; Mismatches 14; Indels 10; Gaps 3;

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DB 1 EVQLVESGGGVQPGGSLRLSCAASGTFSS-YGMHWVRQAPGKLEWVAIRVDGSKNY 59
QY 60 YNPVSKGRITISRDSDSKNTFYLQMSLRADTAIVYCAR-GSHYFGHWHFAVMGQ 114
DB 60 YADSVKGRFTISRDNSKNTLYLQMSLRADTAIVYCAKDLNY-----WGQ 106

RESULT 4
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:25:46 ; Search time 26.6667 Seconds
(without alignments)
353.439 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHHFAVWGQ 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/PCRTUS COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/RG COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	114	1	US-08-887-352B-12
2	625	100.0	114	2	US-09-109-207C-12
3	625	100.0	114	2	US-09-296-005-12
4	625	100.0	114	2	US-09-920-171-12
5	625	100.0	114	2	US-09-716-028-12
6	625	100.0	114	2	US-10-113-996-12
7	625	100.0	229	1	US-08-887-352B-20
8	625	100.0	229	2	US-09-109-207C-20
9	625	100.0	229	2	US-09-296-005-20
10	625	100.0	229	2	US-09-920-171-20
11	625	100.0	229	2	US-09-716-028-20
12	625	100.0	229	2	US-10-113-996-20
13	625	100.0	233	1	US-08-887-352B-25
14	625	100.0	233	2	US-09-109-207C-25
15	625	100.0	233	2	US-09-296-005-25
16	625	100.0	233	2	US-09-920-171-25
17	625	100.0	233	2	US-09-716-028-25
18	625	100.0	233	2	US-10-113-996-25
19	625	100.0	248	1	US-08-887-352B-22
20	625	100.0	248	2	US-09-109-207C-22
21	625	100.0	248	2	US-09-296-005-22
22	625	100.0	248	2	US-09-920-171-22
23	625	100.0	248	2	US-09-716-028-22
24	625	100.0	248	2	US-10-113-996-22
25	625	100.0	451	1	US-08-887-352B-14
26	625	100.0	451	1	US-08-887-352B-16
27	625	100.0	451	2	US-08-466-151-65

28	625	100.0	451	2	US-09-109-207C-14	Sequence 14, Appl
29	625	100.0	451	2	US-09-109-207C-16	Sequence 16, Appl
30	625	100.0	451	2	US-09-296-005-14	Sequence 14, Appl
31	625	100.0	451	2	US-09-296-005-16	Sequence 16, Appl
32	625	100.0	451	2	US-09-920-171-14	Sequence 14, Appl
33	625	100.0	451	2	US-09-920-171-16	Sequence 16, Appl
34	625	100.0	451	2	US-09-716-028-14	Sequence 14, Appl
35	625	100.0	451	2	US-09-716-028-16	Sequence 16, Appl
36	625	100.0	451	2	US-10-113-996-14	Sequence 14, Appl
37	625	100.0	451	2	US-10-113-996-16	Sequence 16, Appl
38	625	100.0	451	2	US-09-925-179-65	Sequence 65, Appl
39	622	99.5	451	2	US-09-925-179-66	Sequence 66, Appl
40	605	96.8	121	1	US-08-887-352B-3	Sequence 3, Appl
41	605	96.8	121	2	US-09-109-207C-3	Sequence 3, Appl
42	605	96.8	121	2	US-09-296-005-3	Sequence 3, Appl
43	605	96.8	121	2	US-09-920-171-3	Sequence 3, Appl
44	605	96.8	121	2	US-09-716-028-3	Sequence 3, Appl
45	605	96.8	121	2	US-10-113-996-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-887-352B-12
; Sequence 12, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-887-352B-12

Query Match          100.0%; Score 625; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSQSYSTGYSWNWIRQAQPKGLEWASITDGS 60
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Db 1 EVQLVESGGGLVQPGGSLRLSCAVSQSYSTGYSWNWIRQAQPKGLEWASITDGS 60
    |||||

Qy 61 NPSVKGRITISRDSDKNTFYLQNSLRAE DTAVYYCARGSHYFGHHFAVWGQ 114
    |||||
Db 61 NPSVKGRITISRDSDKNTFYLQNSLRAE DTAVYYCARGSHYFGHHFAVWGQ 114
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RESULT 2
US-09-109-207C-12
; Sequence 12, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114

RESULT 3
US-09-296-005-12
; Sequence 12, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-296-005-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114
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RESULT 4
US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFPAVWGQ 114

RESULT 5
US-09-716-028-12
; Sequence 12, Application US/09716028
; Patent No. 6723833
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/716,028
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-716-028-12

Query Match      100.0%; Score 625; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.5e-54;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSNNWIRQAPGKLEWVASITYDGSNTY 60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 13:36:22 ; Search time 75.6667 Seconds
(without alignments)
629.505 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARGSHYFGHWHFAVMGQG 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	100.0	114	3	US-09-920-171-12
2	625	100.0	114	4	US-10-113-996-12
3	625	100.0	114	5	US-10-791-619-12
4	625	100.0	114	5	US-10-698-073-5
5	625	100.0	229	3	US-09-920-171-20
6	625	100.0	229	4	US-10-113-996-20
7	625	100.0	229	5	US-10-791-619-20
8	625	100.0	229	5	US-10-698-073-13
9	625	100.0	233	3	US-09-920-171-25
10	625	100.0	233	4	US-10-113-996-25
11	625	100.0	233	5	US-10-791-619-25
12	625	100.0	233	5	US-10-698-073-18
13	625	100.0	248	3	US-09-920-171-22
14	625	100.0	248	4	US-10-113-996-22
15	625	100.0	248	5	US-10-791-619-22
16	625	100.0	248	5	US-10-698-073-15
17	625	100.0	451	3	US-09-920-171-14
18	625	100.0	451	3	US-09-920-171-16
19	625	100.0	451	3	US-09-925-179-65
20	625	100.0	451	4	US-10-113-996-14
21	625	100.0	451	4	US-10-113-996-16
22	625	100.0	451	4	US-10-813-483-4
23	625	100.0	451	4	US-10-813-483-5
24	625	100.0	451	5	US-10-791-619-14
25	625	100.0	451	5	US-10-791-619-16
26	625	100.0	451	5	US-10-714-000-2
27	625	100.0	451	5	US-10-698-073-7

28	625	100.0	451	5	US-10-698-073-9	Sequence 9, Appli
29	625	100.0	451	5	US-10-968-237-65	Sequence 65, Appli
30	625	100.0	451	6	US-11-013-966-4	Sequence 4, Appli
31	625	100.0	451	6	US-11-013-966-5	Sequence 5, Appli
32	625	100.0	669	5	US-10-764-428-21	Sequence 21, Appli
33	622	99.5	451	3	US-09-925-179-66	Sequence 66, Appli
34	622	99.5	451	5	US-10-968-237-66	Sequence 66, Appli
35	605	96.8	121	3	US-09-920-171-3	Sequence 3, Appli
36	605	96.8	121	4	US-10-113-996-3	Sequence 3, Appli
37	605	96.8	121	5	US-10-791-619-3	Sequence 8, Appli
38	605	96.8	453	3	US-09-802-077-8	Sequence 8, Appli
39	605	96.8	453	3	US-09-802-096-8	Sequence 8, Appli
40	605	96.8	453	3	US-09-925-179-8	Sequence 8, Appli
41	605	96.8	453	5	US-10-968-237-8	Sequence 8, Appli
42	603	96.5	114	3	US-09-920-171-11	Sequence 11, Appli
43	603	96.5	114	4	US-10-113-996-11	Sequence 11, Appli
44	603	96.5	114	5	US-10-791-619-11	Sequence 11, Appli
45	603	96.5	114	5	US-10-698-073-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-920-171-12
; Sequence 12, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-920-171-12	Query Match	100.0%;	Score 625;	DB 3;	Length 114;
	Best Local Similarity	100.0%;	Pred. No. 5.3e-51;		
	Matches 114;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	EVQLVESGGGLVQPGGSLRLSCA	VS	YTSITSGYSWMWIR	QAPGKLEWVASITVDGSTNY 60
Db	1	EVQLVESGGGLVQPGGSLRLSCA	VS	YTSITSGYSWMWIR	QAPGKLEWVASITVDGSTNY 60
Qy	61	NPSVKGRITISRDSDSKNTFYLQ	NSLRAEDTAVY	YCARGSHYFGHWHFAVMGQG 114	
Db	61	NPSVKGRITISRDSDSKNTFYLQ	NSLRAEDTAVY	YCARGSHYFGHWHFAVMGQG 114	

RESULT 2

US-10-113-996-12
; Sequence 12, Application US/10113996
; Publication No. US20030149244A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies
; FILE REFERENCE: P1123C3US

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; CURRENT APPLICATION NUMBER: US/10/113,996
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 09/920,171
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-113-996-12

Query Match      100.0%; Score 625; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114

RESULT 3
US-10-791-619-12
; Sequence 12, Application US/10791619
; Publication No. US20040259077A1
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/10/791,619
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/09/109,207
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 12
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-114
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-10-791-619-12

Query Match      100.0%; Score 625; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114

RESULT 4
US-10-698-073-5
; Sequence 5, Application US/10698073
; Publication No. US20050026881A1
; GENERAL INFORMATION:
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; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.201
; CURRENT APPLICATION NUMBER: US/10/698,073
; CURRENT FILING DATE: 2003-10-26
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Humanized Monoclonal Antibody
US-10-698-073-5

Query Match      100.0%; Score 625; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-51;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114

RESULT 5
US-09-920-171-20
; Sequence 20, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 20
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain F(ab) sequence derived from MAE11
US-09-920-171-20

Query Match      100.0%; Score 625; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSNNWIRQAPGKGLEWVASITYDGSNTY 60

Qy 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHHFAVWGQ 114
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 13:37:22 ; Search time 11.6667 Seconds
(without alignments)
92.381 Million cell updates/sec

Title: US-10-791-619-12
Perfect score: 625
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	625	100.0	114	6	US-10-923-327-5
2	625	100.0	229	6	US-10-923-327-13
3	625	100.0	233	6	US-10-923-327-18
4	625	100.0	451	6	US-10-923-327-7
5	625	100.0	451	6	US-10-923-327-9
6	610	97.6	248	6	US-10-923-327-15
7	603	96.5	114	6	US-10-923-327-4
8	603	96.5	229	6	US-10-923-327-14
9	603	96.5	233	6	US-10-923-327-19
10	603	96.5	451	6	US-10-923-327-11
11	598	94.1	248	6	US-10-923-327-16
12	519	83.0	98	7	US-11-084-554-10
13	438	70.1	251	7	US-11-054-515-1114
14	434	69.4	248	7	US-11-054-515-1323
15	432	69.1	248	7	US-11-054-515-835
16	431	69.0	248	7	US-11-054-515-914
17	431	69.0	248	7	US-11-054-515-916
18	427.5	68.4	122	7	US-11-120-338-24
19	427.5	68.4	451	7	US-11-120-338-25
20	427.5	68.4	452	7	US-11-120-338-17
21	427.5	68.4	452	7	US-11-107-028-47
22	427.5	68.4	452	7	US-11-106-820-45
23	424.5	67.9	452	7	US-11-107-028-43
24	424.5	67.9	452	7	US-11-107-028-45
25	424.5	67.9	452	7	US-11-107-028-46

26	424.5	67.9	452	7	US-11-106-820-30	Sequence 30, Appl
27	423.5	67.8	122	6	US-10-771-257-11	Sequence 11, Appl
28	423.5	67.8	122	7	US-11-120-338-8	Sequence 8, Appl
29	423.5	67.8	122	7	US-11-127-677-11	Sequence 11, Appl
30	423.5	67.8	122	7	US-11-107-028-30	Sequence 30, Appl
31	423.5	67.8	122	7	US-11-106-820-8	Sequence 8, Appl
32	423.5	67.8	451	7	US-11-120-338-22	Sequence 22, Appl
33	423.5	67.8	452	7	US-11-120-338-14	Sequence 14, Appl
34	423.5	67.8	452	7	US-11-120-338-15	Sequence 15, Appl
35	423.5	67.8	452	7	US-11-107-028-32	Sequence 32, Appl
36	423.5	67.8	452	7	US-11-107-028-33	Sequence 33, Appl
37	423.5	67.8	452	7	US-11-106-820-26	Sequence 26, Appl
38	423.5	67.8	452	7	US-11-106-820-28	Sequence 28, Appl
39	423.5	67.8	471	7	US-11-106-820-25	Sequence 25, Appl
40	423.5	67.8	471	7	US-11-106-820-27	Sequence 27, Appl
41	423	67.7	251	7	US-11-054-515-955	Sequence 955, App
42	423	67.7	252	7	US-11-054-515-988	Sequence 988, App
43	422	67.5	118	6	US-10-648-816-9	Sequence 9, Appl
44	422	67.5	118	6	US-10-648-816-14	Sequence 14, Appl
45	420.5	67.3	116	7	US-11-127-932-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-923-327-5
; Sequence 5, Application US/10923327
; Publication NO. US20050261208A1
GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROPIANDROSTERONE-SULFATE WITH AN ANTI-IGF
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723-501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-5

Query Match 100.0%; Score 625; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.6e-47;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASITDGSNTY	60
Db	1	EVLVESGGGLVQPGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLWVASITDGSNTY	60
QY	61	NPQVKRITISRDDSKNTFYLOWNSLRADTAVVYCARGSHYFGHWHFAVWGQ	114
Db	61	NPQVKRITISRDDSKNTFYLOWNSLRADTAVVYCARGSHYFGHWHFAVWGQ	114

RESULT 2

US-10-923-327-13
; Sequence 13, Application US/10923327
; Publication NO. US20050261208A1

